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Database :
                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                             389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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68
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Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

esult No.	Score	% Query Match	Length	DB	ij	Description
1	65	95.6	89	4	US-08-618-485B-2	Sequence 2, Appli
N	. 65		94	4.	S-08-618-48	'n
w	65	ū	458	4,	-08-618-	۲
4	65	ū	458	σ	770	51
ហ	59		458	σ	177	Patent No. 5177002
σ.	59	86.8	474	_	US-08-222-619-5	Sequence 5, Appli
7	59		474	տ	04075	ū
œ	41		898	4	9-585-858-3	37, 1
v	39		82	4	-08-311	351,
10	39	•	99	4	US-08-311-731A-76	76
11	39	•	115	4	-08-311	e 295,
12	39	•	496	N	US-08-949-637-2	e 2
13	39	57.4	496	ω	US-09-291-488-2	e 2,
14	39	•	507		US-09-153-277-4	4
15	39	•	695		US-09-153-277-2	Sequence 2, Appli
16	38	•	556		US-08-505-377-1	e 1,
17	38	55.9	556		US-08-798-269-1	e 1,
18	38	•	556		US-09-055-210-1	,,
19	38	55.9	556		US-09-298-924-8	8, Api
20	38	•	749		US-09-489-039A-7979	79
21	37	•	65		US-09-134-001C-4977	49
22	36	•	86	N	US-08-809-740A-3	
23		•	250		-198-452A-	85
24	36		256	4	US-09-134-001C-3271	32
25		•	402	4	US-09-252-991A-20804	20804,
26	36	52.9	970	σ	5229293-2	Patent No. 5229293
د	,		1504	_	115-09-352-7046	Semience 7046 An

45	44	43	42	41	40	39	38	37	36	35	34	y U	32	31	30	29	0
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50.0	50.0	50.0	50.0	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	01.0
243	145	86	60	1531	1527	1525	1160	821	478	322	322	275	275	256	214	174	0.4
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US-09-107-532A-4665	US-09-134-000C-4292	US-09-621-976-6582	US-09-621-976-6141	US-09-418-710-29	US-09-418-710-27	US-09-418-710-69	US-09-328-352-6457	US-08-339-578-2	US-09-134-000C-4712	PCT-US95-13659-2	US-08-327-494A-2	US-09-134-000C-6528	US-09-107-532A-4013	US-08-956-171E-5228	US-09-587-066-6	US-09-107-532A-4968	00-03-010-00-00-00-00-00-00-00-00-00-00-00-00
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Contract
4665, Ap	4292, Ap	6582, Ap	6141, Ap	29, App1	27, App1		6457, Ap	Z, Appli	4712, Ap	2, Appli	2, Appli	6528, Ap	4013, Ap	5228, Ap	6, Appli	4968, Ap	der tono

ALIGNMENTS

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HARACTERISTICS: 89 amino acids mino acid 1 linear TYPE: protein PAL: no DOURCE: 1: Human	5 . 4 2 . 5 . 5 . 5 .	COUNTRY: USA ZIP: 19103-2212 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb COMPUTER: IBM FC Compatible OPERATING SYSTEM: PC COMPUTER: PC COMPUTER: SOFTWARE: WORDPERFECT VERSION 4.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/618,485B PILING DATE: MARCh 19, 1996- CLASSIFICATION: 435	TITLE OF INVENTION: PACKOFFAGE ACTIVATION OF TITLE OF INVENTION: BINDING PROTEIN AND ITS DOMAIN TITLE OF INVENTION: BINDING PROTEIN AND ITS DOMAIN TITLE OF INVENTION: FOR CANCER, HIV-INFECTION AND TITLE OF INVENTION: OSTEOPETROSIS INVENER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSER: CAESAR, RIVISE, BERNSTEIN, ADDRESSER: COHEN & POKOTILOW, LTD. STREET: 1635 MARKET Street, 12th Floor CITY: Philadelphia STATE: PA	485B-2 2, Application US/08618485B 0, 6410269 INFORMATION: CANT: NOBUTO YAMAMOTO CANTINUENTION: PREPARATION OF POTENT OF INVENTION: ACCOUNTED ACTIVATION.

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US-08-618-485B-3
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                                                                                                  TRIEFAX: (215)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 94 amino acids
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6410269
                                               TYPE: aming Inear TOPOLOGY: linear MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 19103-2212
COMPUTER READABLE FORM:
MEDIUM_TYPE: Diskette-3.5 inch, 1.44 Mb
                              HYPOTHETICAL: n
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-JUNE-1995
ATTORNEY/ACENT INFORMATION:
NAME: Robert S. Silver
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: Y1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT VERSION 4.2 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JMBER OF SEQUENCES:
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DATE: December, 1985

RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,681
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/618,485B FILING DATE: March 19, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CAESAR, RIVISE, BERNSTEIN, ADDRESSEE: COHEN & POKOTILOW, LTD. STREET: 1635 Market Street, 12th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
INDIVIDUAL ISOLATE:
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Serum Vitamin D-binding Protein is a Third Member
of the Albumin and Alpha Fetoprotein Gene Family
                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08618485B
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                  Human
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                                                                   protein
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MACROPHAGE ACTIVATING FACTORS
DERIVED FROM CLONED VITAMIN D
BINDING PROTEIN AND ITS DOMAIN
AND THEIR THERAPEUTIC USAGE
FOR CANCER, HIV-INFECTION AND
                                                                                                                                                                                        567-2010
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Vitamin D-binding protein
                                                                                                                                                                                                                          Y1004/20002
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Pred. No. 9.4e-05;
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protein)
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Best Local (
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/618,485B
FILING DATE: MARCh 19, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          TELEFAX: (215) 751-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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AUTHORS: Cooke, Nancy E., David, B Vivek
TITLE: Serum Vitamin D-binding Protein is a Third Member
TITLE: of the Albumin and Alpha Fetoprotein Gene Family
JOURNAL: J. Clinical Investigation
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDLIM TYPE: Diskette-3.5 inch, 1.44
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                             REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2010
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acid
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORDPERFECT VERSION 4.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                 ORIGINAL SOURCE:
                                                             WOLECULE TYPE: p
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CAESAR, RIVISE, BI
ADDRESSEE: COHEN & POKOTILOW
INDIVIDUAL ISOLATE:
                              ORGANISM:
                                                                                                   TOPOLOGY:
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13; Conserv
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                                                                                                              4: 458 amino acids amino acid
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2420-2424
2487, 1985
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                                    Human
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BINDING PROTEIN AND ITS DOMAIN
AND THEIR THERAPEUTIC USAGE
FOR CANCER, HIV-INFECTION AND
OSTEOPETROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACROPHAGE ACTIVATING FACTORS
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 Vitamin D-binding protein (Gc protein)
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Pred. No.
                                                                                                                                                                                                                                 Y1004/20002
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OW, LTD.
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APPLICANT: YAMAMOTO, NOBUTO

TITLE OF INVENTION: IN VIRTO ENZYMATIC CONVERSION OF
GLYCOSLATED HUMAN VITAMIN D BINDING PROTEIN TO A POTENT
MACROPHAGE ACTIVATING FACTOR
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/576,248
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA;
APPLICATION NUMBER: 439,223
FILING DATE: 20-NOV-1989
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                                                                                                                   5177002-2
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MACROPHAGE ACTIVATING FACTOR
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 439,223; FILING DATE: 20-NOV-1989; SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YAMAMOTO, NOBUTO
TITLE OF INVENTION: IN VIRTO ENZYMATIC CONVERSION OF
GLYCOSLATED HUMAN VITAMIN D BINDING PROTEIN TO A POTENT
                                                                                                                                                SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.6%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                     Matches
                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                   LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGES:
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13; Conservative
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Serum Vitamin D-binding Protein is a
Third Member of the Albumin and Alpha
Fetoprotein Gene Family
L: J. Clinical Investigation
TPTELAKLVNKRSE 14
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                                                   Conservative
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                                                                   86.8%;
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                                                                   Score 59; I
Pred. No. 0.
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Pred. No. 0.00056;
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Pred. No. 0.00056;
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0.0071;
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PCT-US95-04075-5
                                                                                                                                                                                                                                                                                  Sequence 5, Application PC/TUS9504075
GENERAL INFORMATION:
APPLICANT: AMGEN INC.
TITLE OF INVENTION: Afamin: A Hum:
TITLE OF INVENTION: Protein
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acid
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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STREET: 1840 DeHavilland Drive
CITY: Thousand Oake
STATE: California
                                                                                                                                                                                   ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                   COUNTRY: U.S.
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Wright, Samuel
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DB 1; Length 474;

Indels

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Gaps

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APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/09/585,858
CURRENT APPLICATION NUMBER: 08/137,120
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
PRIOR PRIOR PRIOR DATE: 1999-06-02
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Best Local Similarity
"hes 7; Conserv?
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US-09-585-858-37
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; ORGANISM: Bacteriophage RB69
US-09-585-858-37
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PCT-US95-04075-5
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SEQ ID NO 37
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Best Local !
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                                                                                                                                                                      APPLICANT: SMITH, DOU
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: N
TITLE OF INVENTION: N
TITLE OF INVENTION: D
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: WOLF, GRE
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Local Similarity 85.7%;
                                                        COUNTRY: U
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TOPOLOGY: unk
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o. 6583266
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                                                                                                         BOSTON
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600 ATLANTIC AVENUE
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                                                                        USA
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                                                                                                                                                                                                            NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
                                                                                                                                                                                            DIAGNOSTICS AND
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Pred. No. 30;
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                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acid-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Best Local Similarity
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TELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: :
                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: GATTES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
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                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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LENGTH: 82 amino acids
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
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SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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MOLECULE TYPE:
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CLASSIFICATION: 530
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                   TYPE: am TOPOLOGY:
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                   amino acid
)GY: linear
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protein
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57.1%;
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                                                                                                                                                                C0044/7125
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Pred. No.
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                                                                                                RESULT 12
US-08-949-637-2
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US-08-311-731A-295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-311-731A-295
                         Sequence 2, Application US/08949637 Patent No. 5910414
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 295,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: GATES EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: pro
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: BOSTON
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ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES ITTLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                          Match 57.4%; Cocal Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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                                                                                                                                                                                                                                         TPTMLAKTLNRVTE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08311731A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae
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 Mismatches

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Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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PRIOR APPLICATION DATA:
APPLICATION UNMER: 60/028,370

PILING DATE: 15-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: 950566

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478

TELEPHONE: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                            APPLICANT: Gwynn, Michael
APPLICANT: Kallendar, Howard
TITLE OF INVENTION: No. 6251387el Topoisomerase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
SOLDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5910414el Topoisomerase I NUMBER OF SEQUENCES: 3
                                                                                 COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,637
FILING DATE: 14-OCT-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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TOPOLOGY: lir
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                                                                                                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
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                                                                     IBM Compatible
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   US/09/291,488
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Pred. No. 37;
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CLASSIFICATION: PRIOR APPLICATION NUMBER:

08/949,637

ATTORNEY/AGENT INFORMATION:

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                                                                                                                        RESULT 15
US-09-153-277-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kallender, Howard
APPLICANT: Gwynn, Michael
APPLICANT: Sylvester, Daniel
APPLICANT: Katz, Lisa
APPLICANT: Katz, Lisa
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 507
                                                                  Sequence 2, Application US/09153277
Patent No. 6331411
GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Query Match 57.4%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/153,277
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 08/949,637
EARLIER FILING DATE: 1997-10-14
APPLICANT: Kallender, Howard
APPLICANT: Gwynn, Michael
APPLICANT: Sylvester, Daniel
APPLICANT: Katz, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: topA FILE REFERENCE: P50566-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Warren, Richard L. APPLICANT: Traini, Christopher M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gimmi, Edward R
REGISTION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 PTELGEIVNK 433
                                                                                                                                                                                              423 PTELGEIVNK 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PTELAKLVNK 11
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                                                                                                                                                                                                                    PTELAKLVNK 11
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                                                                                                                         ; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-153-277-2
                                     Query Match
Best Local Similarity 70.0
                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 695
                                                                                                                                                                                                                  FILE REFERENCE: P50566-01
CURRENT APPLICATION NUMBER: US/09/153,277
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 08/949,637
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                               APPLICANT: Warren, Richard L.
APPLICANT: Traini, Christopher M.
TITLE OF INVENTION: topa
 505 PTELGEIVNK 514
                2 PTELAKLVNK 11
                                                                         57.4%;
                                                                           Score 39; DB 4;
Pred. No. 53;
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Search completed: May 21, 2004, 18:04:17 Job time: 25 secs

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                  1586107 segs, 282547505 residues
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Listing first 45 summaries
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ALIGNMENTS

The present peptide, designated fADP, is derived from domain III of a human vitamin D binding protein. It comprises a sugar residue, especially an N-acetylgalactosamine, attached at the Thr-3 residue, or lacks a sugar moiety. A claimed peptide for increasing bone density in a mammal comprises the first 3-13 amino acids of fADP, or has at least 70% (preferably at least 90%) homology to fADP. The peptide is used in a claimed method for promoting bone deposition. This is useful in the treatment of disorders involving bone loss, particularly osteoporosis, osteogenesis imperfecta, osteopenia, bone fracture, reconstruction of bone after tumour removal to achieve spine and other joint fusion, bone

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RESULT 2
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The present sequence represents the cloned domain III-derived macrophage activating factor (CdMAFI), which is from a vitamin D3 binding protein (GcP). Full length cDNA encoding the human Gc protein, isolated from a human liver cDNA library in bacteriophage lambda, was cloned into a baculovirus expression system to produce the cloned protein recombinantly. GcMAFC, CdMAF and GcMAF (similar to GcMAFC, but prepared from serum rather than recombinant protein) are used to treat cancer, or HIV, Epstein-Barr virus or herpes zoster infection, and to promote bone formation in osteoporosis. They are also adjuvants for immunisation, or vaccination. Alpha-AG is present in all patients with cancer and HIV infection, and its level is inversely correlated with precursor activity of plasma GcP, so measurement of alpha-AG may be useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloned Gc protein-macrophage activating factor; human; baculovirus; cancer; viral infection; osteoporosis; immunisation; vaccination; HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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19-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and osteoporosis treatment.
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                                                                                                                         The present sequence represents the cloned domain III-derived macrophage activating factor (cdMAF2), which is from a vitamin D3 binding protein (GcP). Full length cDNA encoding the human Gc protein, isolated from a human liver cDNA library in bacteriophage lambda, was cloned into a baculovirus expression system to produce the cloned protein recombinantly. GcMAFC, CdMAF and GcMAF (similar to GcMAFC, but prepared from serum rather than recombinant protein) are used to treat cancer, or HIV, Epstein-Barr virus or herpes zoster infection, and to promote bone formation in osteoporosis. They are also adjuvants for immunisation, or vaccination. Alpha-AG is present in all patients with cancer and HIV infection, and its level is inversely correlated with precursor activity of plasma GcP, so measurement of alpha-AG may be useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                 Cloning vitamin D3 binding protein or its domain III in baculovirus - produce macrophage activating factors, useful in cancer, viral infect:
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                                   Gaps
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                                                     Matches
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Best Local S
                                                                                                                              The vitamin D binding protein Gcl is an evolutionary conserved glycoprotein. Polymorphism of the Gc protein was demonstrated by gel electrophoretic analysis, which revealed two major phenotypes: Gcl and Gc2 (AAR22279). The Gc protein may be purified by a variety of means from blood, e.g. by 25-hydroxy vitamin D3-Sepharose affinity chromatography. Gcl may be converted to MAF by the action of glycosidases of B and T cells, e.g. by contacting Gcl in vitro with beta-galactosidase or beta-gal in combination with sialidase and/or alpha-mannosidase. The MAF may be produced in large amts. with high potency. MAF may be used for inducing macrophage activation, partic. in patients with immunodeficient diseases, cancer and other diseases characterised by impaired B- or T-cell fuction
                                                                                                                                                                                                                                                                                                                                         Prepn. of new macrophage activating factor - by contacting human gp.-specific component with glycosidase(s), useful for treating immunodeficient diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macrophage activating factor; MAF; galactosidase; sialidase; mannosidase; B cells; T cells; cancer; immunodeficient diseases; Vitamin D binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-114364/14
                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9204459-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gp.-specific component phenotype Gc1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR22278 standard; protein; 458
                                                                                                         Sequence 458
                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                Local Similarity
418
               1 TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAMAMOTO N.
TPTELAKLVNKRSD 431
                                                     Conservative
                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91WO-US006172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Asp in Gc2"
420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Glu in Gc2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Gly in Gc2"
                                                                95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Lys in Gc2'
                                                    Score 65; DB 2;
Pred. No. 0.0013;
1; Mismatches
                                                     0
                                                                              Length 458;
                                                      Indels
                                                     0
                                                      Gaps
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RESULT 5
AAR56975
ID AAR5

AAR56975 standard; protein; 458 AA.

Vitamin D3-binding protein GcMAFc from cloned

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protein.

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RESULT 6
AAW10561
ID AAW1
XX
AC AAW1
XX
AC AAW1
XX
AC 24-S
XX
DE Vita
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                                                                                                                                                                                                                                                                                                                                                                                       CC Vitamin D binding protein (DBP) is converted to a macrophage activating CC factor by the action of B and T cell glycosidases. The polymorphic DBP CC phenotypes are expressed inter alia as differences in the oligosaccharide CC attached to the polypeptide portion of the DBP molecule. All three CC principal DBP types - DBPgm, DBPgs and DBPg differ in the nature of the cappended oligosaccharide. DBPgs which possesses an oligosaccharide moiety CC which includes galactose and sialic acid residues can be converted to the CC macrophage activating factor by contact with beta-galactosidase and CC sialidase. DBPgm which is believed to possess an oligosaccharide moiety CC which includes galactose and alpha-mannose residues is contacted with beta-galactosidase and alpha-mannose residues is contacted with beta-galactosidase and coligosaccharide moiety CC oligosaccharide moiety which is believed to possess an oligosaccharide moiety which is believed to possess an oligosaccharide coligosaccharide moiety which is believed to possess an oligosaccharide moiety which is believed to possess an oligosaccharide moiety which is believed to possess an oligosaccharide moiety which includes galactosidase alone to form the CC oligosaccharide moiety which includes galactose without sialic acid or Clopace is contacted with beta-galactosidase alone to form the CC macrophage activating factor. The resulting factor is of high potency. CC (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1989;
31-AUG-1990;
30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vitamin D binding protein; DBP; macrophage activating factor; oligosaccharide; galactose; alpha mannose; sialic acid; beta-galactosidase; alpha-mannosidase; sialidase; MAF.
                                                                                                                                                                                                                                                                                                                                                          Sequence 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macrophage activating factor - prepared by treating glycosated vitamin D-binding protein with glycoside(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5326749-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variant vitamin D binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
16-FEB-1995
                                                      24-SEP-1997
                                                                                                                        AAW10561 standard; protein; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-217073/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR56975;
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                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                     1 Similarity
                                                                                                                                                                                                                  TPTELAKLVNKRSD 431
                                                                                                                                                                                                                                      TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                            Ŗ,
                                                  (first entry)
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(first entry)
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90US-00576248.
91US-00767742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-00000320
                                                                                                                                                                                                                                                                                                      95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (DBPgs/gm)
                                                                                                                                                                                                                                                                                   Score 65; DB 2;
Pred. No. 0.0013;
1; Mismatches
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                         Length 458;
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RESULT 7
ABP58017
ABP58017
ABP58017
XX
AC ABP5
XX
DT 11-I
XX
DT 11-I
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Hum
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KW Pro

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Matches 13
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                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vitamin D3 binding protein or its domain III in baculovirus - to produce macrophage activating factors, useful in cancer, viral infection and osteoporosis treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                         Prostate cancer; marker; vitamin D binding protein; VDBP; human; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 458 AA;
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19-MAR-1996;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human serum vitamin D binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP58017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YAMA/) YAMAMOTO
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                                                                                                                             Peptide
                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418
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13; Conserv
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96US-00618485.
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                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                       /note=
                                                      . 94
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                                                                                   "marker peptide"
                                                                                                                                                                   "marker peptide"
            "marker peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 2; Lo
Pred. No. 0.0013;
1; Mismatches 0;
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RESULT 8
AAR22279
ID AAR2
XX
AC AAR2
XX
AC AAR2
XX
AC AAR2

AAR22279 standard;

protein;

458

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27-JUL-1992 AAR22279;

(first entry)

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                                                  Matches
                                                                           Query Match
                                                                                                                          The present sequence is the protein sequence of an allele of human human serum vitamin D binding protein (VDBP). The invention provides a novel human protein that includes amino acid sequences (see ABPS805-16) that are also found in VDBP. These marker sequences can be used to distinguish VDBP-related proteins from other proteins. VDBP-related proteins are detectable at a higher concentration in serum from a mammal, e.g. a human, with prostate cancer relative to serum from a healthy mammal and can therefore be used as prostate cancer markers. They permit the rapid detection, preferably before metastases occur, of prostate cancer. A target prostate cancer-associated protein may be detected using a prostate cancer-associated protein, and nucleic acids encoding them, are also useful as targets for treating prostate cancer, and as indicators for monitoring the efficiency of prostate cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                         Diagnosing or treating prostrate cancer by detecting in a sample isolated from the individual the presence of prostate cancer-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-067369/06.
N-PSDB; ABV76007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                     Sequence 474
                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hlavaty J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-2001; 2001WO-US045031.
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                                                                Local
434 TPTELAKLVNKHSD 447
                                                  12;
                       1 TPTELAKLVNKRSE 14
                                                                Similarity
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                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
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                                                                88.2%;
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.363
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                                                                Score 60; DB 6;
Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide"
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                                                    Mismatches
                                                                            DB 6;
                                                                             Length 474;
                                                      Indels
                                                      0,
                                                      Gaps
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Human

gp.-specific component phenotype Gc2

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RESULT 9
AAR56976
ID AAR5
XX
XX
AC AAR6
DT 25-h
DT 16-1
XX
DE Vari
                                                                                                                                                                                                                                                                           #XFFFX8X555555555555555555555555
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                                                                                                                                                                                      S
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                               The vitamin D binding protein GC2 is an evolutionary conserved glycoprotein. Polymorphism of the GC protein was demonstrated by gel electrophoretic analysis, which revealed two major phenotypes: GC1 (ARR2278) and GC2. The GC protein may be purified by a variety of means from blood, e.g. by 25-hydroxy vitamin D3-Sepharose affinity chromatography or actin-agarose affinity chromatography. GC1 may be converted to MAF by the action of glycosidases of B and T cells, e.g. by contacting GC1 in vitro with beta-galactosidase or beta-gal in combination with sialidase and/or alpha-mannosidase. The MAF may be produced in large amts. with high potency. MAF may be used for inducing macrophage activation, partic. in patients with immunodeficient diseases, cancer and other diseases characterised by impaired B- or T-cell fuction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macrophage activating factor; MAF; galactosidase; sialidase; mannosidase; B cells; T cells; cancer; immunodeficient diseases; Vitamin D binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepn. of new macrophage activating factor - by contacting human gp.-
specific component with glycosidase(s), useful for treating immuno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-114364/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deficient diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9204459-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
Variant vitamin D binding protein (DBPg).
                           25-MAR-2003
16-FEB-1995
                                                                   AAR56976;
                                                                                           AAR56976 standard; protein; 458 AA
                                                                                                                                                                                                                                                                         Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YAMA/) YAMAMOTO N.
                                                                                                                                                                 418
                                                                                                                                                                                                                 l Similarity
12; Conserv
                                                                                                                                                                                        1 TPTELAKLVNKRSE 14
                                                                                                                                                                 TPKELAKLVNKRSD 431
                                                                                                                                                                                                                    Conservative
                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-00576248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Gly in Gc2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Glu in Gc2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Lys in Gc2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Asp in Gc2"
                                                                                                                                                                                                                                86.8%;
                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                 Score 59;
Pred. No.
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                   0.018;
                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                              Length 458;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                    0
                                                                                                                                                                                                                    Gaps
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Homo sapiens.

DE19813835-A1

Expressed sequence tag; EST; human; breast; cancer; cytostatic; medicaments; gene therapy; treatment; fat metabolism.

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RESULT 10
AAY48469
ID AAY48
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                                                                                                                                                                                                                                                                                                                                                                                                  Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vitamin D binding protein (DBP) is converted to a macrophage activating. CC factor by the action of B and T cell glycosidases. The polymorphic DBP CC phenotypes are expressed inter alia as differences in the oligosaccharide attached to the polypeptide portion of the DBP molecule. All three CC principal DBP types - DBPgm, DBPgs and DBPg differ in the nature of the cuppended oligosaccharide. DBPgs which possesses an oligosaccharide moiety CC which includes galactose and sialic acid residues can be converted to the CC macrophage activating factor by contact with beta-galactosidase and CC which includes galactose and alpha-mannose residues is contacted with beta-galactosidase and alpha-mannose residues is contacted with beta-galactosidase and alpha-mannose residues is contacted with beta-galactose without sialic acid or clipseaccharide moiety which is believed to possess an oligosaccharide coligosaccharide moiety which is believed to possess an coligosaccharide moiety which is believed to possess an clipseaccharide moiety which his believed to possess an clipseaccharide moiety which his believed to possess an coligosaccharide moiety which his believed to possess an clipseaccharide moiety which his believed to possess an clipseaccharide moiety which his believed to possess an clipseaccharide moiety which his believed to possess an clipseaccharide.)

CC clipha-mannose is contacted with beta-galactosidase alone to form the cc macrophage activating factor. The resulting factor is of high potency.

CC (Updated on 25-MAR-2003 to correct PF field.)
X A X E X E X B X S X E X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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31-AUG-1990;
30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitamin D binding protein; DBP; macrophage activating factor; oligosaccharide; galactose; alpha mannose; sialic acid; beta-galactosidase; alpha-mannosidase; sialidase; MAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macrophage activating factor - prepared by treating glycosated vitamin binding protein with glycoside(\epsilon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-217073/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YAMA/) YAMAMOTO N.
                                                                                                                                               Human breast tumour-associated protein 14.
                                                                                                                                                                                        08-DEC-1999
                                                                                                                                                                                                                            AAY48469;
                                                                                                                                                                                                                                                                 AAY48469 standard; protein; 314
                                                                                                                                                                                                                                                                                                                                                                418
                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 85.
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    1 TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                  TPKELAKLVNKRSD 431
                                                                                                                                                                                        (first entry)
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90US-00576248.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59; DB 2;
Pred. No. 0.018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 458;
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biodiversity

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RESULT 11
ABG15879
ID ABG15879
AC ABG15
XX ABG15
AC ABG15
XX ABG16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel human nucleic acid sequences from normal breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer and for treating illnesses associated with fat metabolism. AAY48456-Y48339 represent protein fragments encoded by the expressed sequence tags described in the method of the invention
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N-PSDB; AAZ33550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG15879 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 314 AA;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS80066.
                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #15870
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                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
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                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                         2000US-00540217.
2000US-00649167.
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                                                                                                                                                                                    Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches
                                                                                                                                                23-APR-2001;
27-APR-2001;
05-JUN-2001;
09-JUL-2001;
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ25543;
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                                                                                                                                                                                                                                            23-APR-2002; 2002WO-US013142
                                                                                                                                                                                                                                                                           31-OCT-2002.
                                                                                                                                                                                                                                                                                                         WO200286090-A2
                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                   Fungicide; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus fumigatus essential gene protein #201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ25543 standard; protein; 705 AA.
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                                                           WPI; 2003-093124/08.
                                                                                        Jiang B,
                                                                                                                       (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                      contamination;
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                                                                                                                       ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSELRNLVNKHSE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTELAKLVNKRSE 14
                                                                                        Tishkoff D,
                                                                                                                                                ; 2001US-0285697P.
; 2001US-0287066P.
; 2001US-0295890P.
; 2001US-0303899P.
; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%;
                                                                                                                                                                                                                                                                                                                                                                     essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
                                                                                        Zamudio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
Pred. No.
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                                                                                           Broshkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 13;
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                                                                                           Lemieux
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New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.

Disclosure; Page; 175pp;

English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                               23-APR-2001;
27-APR-2001;
05-JUN-2001;
09-JUL-2001;
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel purified or isolated nucleic acids essential genes of Aspergillus fumigatus. The isolated nucleic acide the invention are used to treat or prevent infections by a pathogo organism such as A. fumigatus, to treat a non-infectious disease i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 705
                                                          Jiang B,
                                                                                                                                                                                                                                                                                                                                                                    23-APR-2002; 2002WO-US013142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200286090-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungicide; cytostatic;
cancer; contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus fumigatus essential gene protein #801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ26143;
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                                                                                                                       (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 64.: 9; Conservative
                                                                                                                       ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPADLAKLAELRSE 575
                                                          Tishkoff D,
                                                                                                                                                                               ; 2001US-0285697P.
; 2001US-0287066P.
; 2001US-0295890P.
; 2001US-0303899P.
; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
                                                             Zamudio
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Pred. No. 31;
1; Mismatches
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                                                             Broshkin AM,
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New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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Disclosure; Page; 175pp; English.

pathogenic

in a

acids of

cc subject (e.g. cancer), to prevent or contain contamination of an object CC by A. fumigatus, or to prevent or inhibit formation on a surface of a CC biofilm comprising A. fumigatus. The polynucleotides are useful for CC expressing recombinant protein for characterisation, screening or CC therapeutic use, as markers for host tissues in which the pathogenic CC organisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or CC similar biochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and CC making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an CC antigen to raise anti-DNA antibodies or to elicit another immune cresponse, and for identifying polynucleotides encoding the other protein continuous cont The invention relates to novel purified or isolated nucleic acids essential genes of Aspergillus fumigatus. The isolated nucleic ac the invention are used to treat or prevent infections by a pathog organism such as A. fumigatus, to treat a non-infectious disease nucleic acids of ted nucleic acids of pathogenic

Sequence 748 AA;

S Matches Query Match Best Local 1 TPTELAKLVNKRSE 14 9 Similarity Conservative 64.3%; Score 43; DB Pred. No. 33; Mismatches 4: Indels 0, Gaps 0

6

Length 748;

RESULT 14 AAB46728

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TPADLAKLAELRSE 618

AAB46728 standard; protein; 898

AAB46728;

11-SEP-2003 12-APR-2001 (revised) (first entry)

Bacteriophage RB69 DNA polymerase protein fragment SEQ ID ğ 37.

Genome; thermophilic enzyme; washing powder; bleaching

Enterobacteria phage RB69

WO200075335-A2

14-DEC-2000.

02-JUN-2000; 2000WO-IB000893

02-JUN-1999; 99US-0137120P

(DECO-) DECODE GENETICS EHF.

Hjorleifsdottir S, Kristjansson JK; Hreggvidsson GO, Fridjonsson OH, Aevarsson A;

in recombinant DNA technology.

Isolated nucleic acid from bacteriophage RM 378 encoding enzymes useful

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RESULT 15
ABB91986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel isolated nucleic molecule (I) comprising CC the genome of bacteriophage RM 378. The invention also describes (I) an CC isolated nucleic acid which encodes a polypeptide obtainable from CC bacteriophage RM 378, or its active derivative or fragment; (2) an CC isolated bacteriophage RM 378 (II); (3) a DNA construct (III) comprising CC contive derivative or fragment sequence; (4) a host cell comprising CC contive derivative or fragment. Bacteriophage RM 378 is useful for CC producing thermophilic enzymes useful in DNA research and commercial CC settings (e.g. proteases and lipases used in washing powder, hydrolytic enzymes used in bleaching). The isolated nucleic acid molecules and CC vectors are useful in the manufacture of encoded polypeptide, as probes CC for isolating homologous sequences (e.g. from other bacteriophage in a CC culture of host cells. The polypeptides can be used as a molecular weight CC marker on SDS-PAGE gels or on molecular sieve gel filtration columns. CC marker on SDS-PAGE gels or or nonlecular sieve gel filtration columns. CC more thermostable than those of other (e.g. mesophilic) bacteriophages is at thermophile, comparature conditions which would be prohibitive for or their enzymes, thus concentrative conditions which can be employed not only in DNA creasarch but also in commercial settings. (Updated on 11-SEP-2003 to
   Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 898 AA;
Identifying plant target proteins for herbicidally active compounds
                                                                                                                            28-AUG-2001; 2001WO-EP009892
                                                                                                                                                           28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                           07-FEB-2002.
                                                                                                                                                                                                                          WO200210210-A2.
                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                    Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                  Herbicidally active polypeptide SEQ ID NO 1197.
                                                                                                                                                                                                                                                                                                                                                  31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                 ABB91986;
                                                                                                                                                                                                                                                                                                                                                                                                               ABB91986 standard; protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3A-P; 42pp; English.
                                 WPI; 2002-269010/31.
                                                              Tietjen K,
                                                                                              (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472
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                                                              Weidler M;
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Best Local (
                                      Matches
                                                                                                                                                             The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful as identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                      comprising aligning and from plant with nucleic organisms.
                                                                                                                 Sequence 1124 AA;
                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 1197; 261pp + Sequence Listing; English.
2 PTELAKLVN 10
                                     Similarity
8; Conserv
                                     Conservative
                                                      58.8%;
                                                                                                                                                                                                                                                                                                                                                                                             comparing nucleic acid or amino acid sequences acid or amino acid sequences from non-plant
                                      0,
                                                        Score 40; DB 5;
Pred. No. 1.9e+02;
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                                                                          Length 1124;
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Search completed: May 21, 2004, 18:01:52 Job time : 57 secs

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Result
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Maximum DB seq length: 200000000
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                                            Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/JUS06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/JUS06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/JUS06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/JUS07 NEW PUB.pep:*

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7: /cgn2 6/ptodata/2/pubpaa/JUS08 PUBCOMB.pep:*

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19: /cgn2 6/ptodata/2/pubpaa/JUS10 PUBCOMB.pep:*

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(without alignments)
92.974 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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    15 US-10-045-673A-1
US-09-826-463-2
US-09-826-463-3
US-09-826-463-1
US-09-826-463-1
US-09-98-909-14
US-10-128-714-3201
US-10-128-714-8201
US-10-369-493-20429
US-10-369-493-714-8201
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Sequence 1, Appli
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Sequence 14, Appl
Sequence 34177, A
Sequence 3201, Ap
Sequence 20429, A
Sequence 196, App
Sequence 17, Appl
Sequence 37, Appl
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250	212	178	79	62	51	1820	1820	1230	692	588	506	493	1946	1750	729	729	711	327	259	216	151	1161	1029	865	710	709	701	61	898
15	12	12	12	11	12	15	15	14	12	14	15	12	12	12	15	12	12	15	14	14	9	15	12	12	15	12	12	14	14
-10-289-762-859	-10-424-5	-10-282-122A-7186	-10-424-5	US-09-864-408A-6676	-10-424-599-16	0-369-493-59	-10-369-493-527	-524-	-10-282-122A	US-10-213-990-6	US-10-108-260A-4387	-10-425-1	US-10-282-122A-62947	-10-243-55	-10-369-493-236	-10-282-122A-5	US-10-282-122A-73062	-10-369-493-30	10-234-432-	US-10-234-432-28	09-969-384-	-10	-10-424-599	-10-425-114	-10-369-4	-10-282-122A-7	-10-282-1	US-10-097-111-397	US-10-270-846-37
Sequence 859, App	e 230315	æ	e 192519,	æ	e 164190	e 5900,	e 52	6	0	о 6,	æ	e 57893	ø	920,	•	56	73062,	e 30	e 31	e 28	22,	e 36		e 55769,	Sequence 18415, A	e 74	e 74	e 39	Sequence 37, Appl

ALIGNMENTS

RESULT 1 US-10-045-673A-1

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Sequence 1, Application US/10045673A

| Publication No. US20030229014A1 |
| GENERAL INFORMATION: Schmeider, Gary B |
| APPLICANT: Depoif, Steven N |
| APPLICANT: Depoif, Steven N |
| APPLICANT: Popoif, Steven N |
| APPLICANT: NOBUTO YAMAMOTO |
| APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: AP
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US-09-826-463-2
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Best Local &
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APPLICATION NUMBER: US/09/826,463

FILING DATE: 05-Apr-2001

CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/618,4858

FILING DATE: March 19, 1996

APPLICATION NUMBER: US 08/478,121

FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Robert S. Silver
REGISTRATION NUMBER: 35,681
REPERENCE/DOCKET NUMBER: Y1004/20002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2010
TELEPAX: (215) 751-1142
               COUNTRY: USA
ZIP: 19103-2212
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT VERSION 4.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 2420-2424

DATE: December, 1985

RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 4 and 5

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PREPARATION OF POTENT
MACROPHAGE ACTIVATING FACTORS
DERIVED FROM CLONED VITAMIN D
BINDING PROTEIN AND ITS DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NOBUTO YAMAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                          ADDRESSE: CAESAR, RIVISE, BEKNSIELL, ADDRESSEE: CAESAR, RIVISE, BEKNSIELL, COHEN & POKOTILOW, LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CAESAR, RIVISE, BERNSTEIN,
COHEN & POKOTILOW, LTD.
STREET: 1635 Market Street, 12th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                  STATE:
                                                                                                                                                                                                 CITY: Philadelphia
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APPLICATION NUMBER: US/09/826,463
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Pred. No. 0.00041;
1; Mismatches 0
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US-09-826-463-1
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Matches
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APPLICANT: NOBUTO YAMAMOTO
TITLE OF INVENTION: PREPARA
                                                                                              APPLICATION NUMBER: US/09/826,463
FILING DATE: 05-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/618,485B
FILING DATE: March 19, 1996
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT S. 511ver
REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: Y1004/20002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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DATE: December, 1985

RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 10 TO 94
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/618,485B FILING DATE: MARCH 19, 1996
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-UNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT VERSION 4.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Robert S. Silver
REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: Y1004/20002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <U
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103-2212
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                           TELEPHONE: (215) 567-2010
TELEFAX: (215) 751-1142
JOURNAL: J. Clinical Inve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (215)
JOURNAL: J. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1635 Market Street, 12th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CAESAR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (215) 567-2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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92.9%;
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J. Clinical Investigation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAESAR, RIVISE, BERNSTEIN, COHEN & POKOTILOW, LTD.
                                               Clinical Investigation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREPARATION OF POTENT
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Pred. No. 0.00043;
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                                                    OTHER INFORMATION: MAP TO AJ009613.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: SWISSPROT HIT: Q04279, EVALUE 2.10e+00
US-10-029-386-34172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-14
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34172, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hlavaty, John
APPLICANT: Briggman, Joseph
TITLE OF INVENTION: Detection and Treatment
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 34172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/0998909 Patent No. US20020164664A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                  Query Match
                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel David R.
APPLICANT: Hanzel David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,284
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                           FEATURE:
                                                                                                                                                                                             ENGTH: 58
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RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1-485
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418
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85.7%;
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69.2%;
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Pred. No. 0.0025;
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Pred. No. 0.
 Score 44;
Pred. No.
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   DB 14;
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                  Length 58;
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US-10-128-714-8201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Aspergillus fumigatus US-10-128-714-3201
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3201
LENGTH: 705
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GENERAL INFORMATION:
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Matches 9; Conserv
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APPLICANT: Hu, Wendi
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
FULE REFERENCE: 10182-018-999
FULE REFERENCE: 10182-018-999
FULE REFERENCE: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                          APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jiang, APPLICANT: Hu, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
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Pred. No.
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US-10-128-714-8201
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SEQ ID NO 20429
LENGTH: 406
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SEQ ID NO 8201
LENGTH: 748
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Publication No. US20040005599A1
GENERAL INFORMATION:
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Best Local Similarity
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SOFTWARE: Pat
SEQ ID NO 196
LENGTH: 856
                                                    APPLICANT: Schoenbrunner, Nancy
APPLICANT: Schoenbrunner, Nancy
APPLICANT: Schoenbrunner,
APPLICANT: Gelfand, David
APPLICANT: Gelfand, David
TITLE OF INVENTION: THERMOSTABLE OR THERMOACTIVE DNA POLYMERASE MOLECULES
TITLE OF INVENTION: WITH ATTENUATED 3'-5' EXONUCLEASE ACTIVITY
FILE REFERENCE: 21314-US1
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/10/401,403
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2002-04-02
NUMBER OF SEQ ID NOS: 203
NUMBER OF SEQ ID NOS: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OP INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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ublication No. US20030233675A1
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                                          PatentIn version 3.2
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Pred. No. 34;
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APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
ITILE OF INVENTION: Bacteriophage RM378 of a Thermophilic
ITILE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/10/270,878
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/9/585,858
PRIOR APPLICATION NUMBER: US/9/585,858
PRIOR APPLICATION NUMBER: US/9/585,858
PRIOR APPLICATION NUMBER: US/09/585,858
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US-10-401-403-196
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US-10-270-875-37
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TYPE: PRT
; ORGANISM: Bacteriophage RB69
US-10-270-875-37
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CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches
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Best Local Similarity
Matches 7; Conserv
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ORGANISM: Bacteriophage RB69
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APPLICANT: Jakob K. Kristjanson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
TITLE OF INVENTION: 1,001-001
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Olafur H. Fridjonsson
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Pred. No. 1.2e+02;
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Query Match Best Local Similarity

53.8%;

Score 41; DB 14; Length 898; Pred. No. 1.2e+02;

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TYPE: PRT
ORGANISM: Bacteriophage RB69
US-10-270-786-37
                                          US-10-270-710-37
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Query Match
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                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/270,710
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
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CURRENT ETLING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
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APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
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APPLICANT: Gudmundur O. Hreggvidss
APPLICANT: Olafur H. Fridjonsson
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TYPE: PRT
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No. US20030087392A1
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Olafur H. Fridjonsson
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60.3%; Score 41; DB 14;
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CURRENT APPLICATION NUMBER: US/10/270,859
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
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LENGTH: 898
TYPE: PRT
ORGANISM: Bacteriophage RB69
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APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
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APPLICANT: Gudmundur O. Hreggvidss
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R;Braun, A.; NOFLEY, Biochim. Biophys. Act A;Title: Sequence and A;Reference number: A;Accession: S39787 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-431,'E'	A;Title: Serum vitami A;Reference number: A: A;Reference number: A: A;Accession: A92765 A;Molecule type: mRNA A;Residues: 1-167.'E; A;Cross-references: G A;Experimental source	A;Accession: A29096 A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-19 <yan2> A;Cross-references: GB:M17156; R;Cooke, N.E.; David, E.V. J. Clin. Invest. 76, 2420-2424,</yan2>	A; Reference number: 1-431, E., 433-435, I. A; Cross-references: GB: L10641, NII A; Experimental source: allele Gc1 R; Yang, F.; Naberhaus, K.H.; Adril Gene 54, 285-290, 1987 A; Title: The vitamin D-binding property of the property o	A; Experimental Source: allete GCZ R; Witke, W.F.; Glbbs, P.E.M.; Zielii Genomics 16, 751-754, 1993 A; Title: Complete structure of the l A; Reference number: A46759; MUID:93; A; Accession: A46759 A; Status: nucleic acid sequence not A; Molecule type: DNA	C; Species: Aumo Baghens (Mail) C; Date: 28-May-1986 #sequence: C; Accession: A94076; A46759; Ā. R; Yang, F.; Brune, J.L.; Naylo; Proc. Natl. Acad. Sci. U.S.A. A; Title: Human group-specific A; Reference number: A94076; MU A; Reference number: A94076; MU A; Accession: A94076 A; Molecule type: mRNA A; Residues: 1-474 < YAN1> A; Cross-references: GB: X33178;	RESULT 1 VYHUD Vitamin D- NiAlternat	ሀርሀሀሀሀሀሀ ፋፋፋፋፋ ሀፋሀ 8 C 8 G O 1 C U G ፋ U
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Riperam, A.; NOLLEY, A.; MUDAWHELZ, S.; CLEVE, A.; Biochim. Biophys. Acta 1216, 385-394, 193 A;Title: Sequence and organization of the human vitamin A;Reference number: 839787; MUID:94092730; PMID:7505619 A;Accession: 839787 A;Status: greliminary A;Residues: 1-431,'E',433-435,'T',437-474 <bra></bra>	A,Title: Serum vitamin D-binding protein is a thirk A;Reference number: A92765; MUID:86086396; PMID:24: A;Recession: A92765 A;Rocession: A92765 A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-167,'E',169-326,'R',328-431,'E',433-4 A;Residues: 1-167,'E',169-326; NII:9181481; PIDN:AJ A;Experimental source: allele GC1 A;Experimental source: allele GC1	A; Accession: A29096 A; Status: translation not shown A; Status: translation not shown A; Molecule type: DNA A; Residues: 1-19 < YAN2> A; Residues: 1-19 < YAN2> A; Residues: 1-19 < YAN2> A; Cross-references: GB:M17156; NID:g181489; PIDN:AJ A; Crooke, N.E.; David, E.V. J. Clin. Invest. 76, 2420-2424, 1985	A; Kesloues: 1-431, E, (433-435, I, 437-414 KHILDA; A; Keross-references: GB:L10641; MID:g340281; PIDN:A; A; Experimental source: allele Gcl R; Yang, F.; Naberhaus, K.H.; Adrian, G.S.; Gardella Gene 54, 285-290, 1987 A; Title: The vitamin D-binding protein gene contain A; Title: The vitamin D-binding brotein gene contain A; Title: The vitamin B;	nski, R. numan Go 315171; shown;	vision 28-May-1986 096; A92765; S3978; S.L.; Cupples, R.I. 7994-7998, 198 r mponent (Ge) is a r :86068030; PMID:241	ALIGNMENTS RESULT 1 VYHUD Vitamin D-binding protein precursor [validated] - human Vitamin D-binding protein precursor [validated] - human C.Scotlan Vern salens (Grejlobulin; group-specific component	F84780 A84534 A86020 S47708 A98174 A46601 A16325 A747835 AC1234 AI1596 A82549 A825773 A53183
tamin D-binding protein gene. 05619	A,Title: Serum vitamin D-binding protein is a third member of the albumin and alpha level, reference number: A92765, MUID:86086396; PMID:2416779 A,Accession: A92765 A,Molecule type: mRVA A,Molecule type: mRVA A,Cross-references: GB:M12654; NID:9181481; PIDN:AAA52173.1; PID:9181482 A,Cross-references: GB:M12654; NID:9181481; PIDN:AAA52173.1; PID:9181482 A,Experimental source: allele GC1		A; KeBLQUES: 1-411, E; /435-435, I; /437-474; FIDN:AAA61704.1; PID:g639896 A; Cross-references: GB:Lilo641; NID:g340281; PIDN:AAA61704.1; PID:g639896 A; Experimental source: allele Gc1 A; Experimental source: allele Gc1 R; Yang, F:, Naberhaus, K.H.; Adrian, G.S.; Gardella, J.M.; Brissenden, J.E.; Bowman, B.] Gene 54, 285-290, 1987 A; Title: The vitamin D-binding protein gene contains conserved nucleotide sequences that A; Reference number: A29096; MUID:88005794; PMID:2958390	; Yang, F.; Bowman, B.H.; Dugaiczyk, A.; gene: differences and similarities between PMID:8325650 translation not shown	C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 17-Mar-2000 C;Date: 28-May-1986 #sequence revision 28-May-1986 #sequence revision 28-May-1986; A90427; A03237 C;Accession: A94076; A46759; A29096; A92765; S39787; A24066; A90427; A03237 R;Yang, F; Brune, J.L.; Naylor, S.L.; Cupples, R.L.; Naberhaus, K.H.; Bowman, B.H. Proc. Natl. Acad. Sci. U.S.A. 82, 7994-7998, 1985 A;Title: Human group-specific component (Ge) is a member of the albumin family. A;Reference number: A94076; MUID:86068030; PMID:2415977 A;Accession: A94076; MUID:86068030; PMID:2415977 A;Accession: A94076 MUID:86068030; PMID:2415977 A;Accession: A94076 MUID:86068030; PMID:2415977 A;Residues: 1-474 < YAN1> A;Residues: 1-474 < YAN1> A;Cross-references: GB:X03178; GB:M11321; NID:g31675; PIDN:CAA26938.1; PID:g31676	human c component	hypothetical prote hypothetical prote hypothetical prote hypothetical follow hypothetical follow hypothetical follow hypothetical prote sarafotoxin precur epidermal growth follow hypothetical prote hypothetical prote DNA topoisomerase DNA topoisomerase phage-related protephage-related protepidermal growth for the poisoner hypothetical protephage related protepidermal growth for the protepidermal growth for the hypothetical protephage related prot

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R;Liu, J.; Yu, K.; Chen, H.; Weng, S. Biochem. Biophys. Res. Commun. 219, 868-875, 1996 A;Title: Regulatory region with putA gene of proline dehydrogenase that links A;Reference number: JC4661; MUID:96216743; PMID:8645272 A;Accession: JC4661
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A;Residues: 17,'Q',19-21,'N',23-36,'XXX',40-41;472-474 <SVN>
G;Comment: DBP is a multifunctional protein found in plasma, ascitic fluid, cerebrospina nts polymerization of actin by binding its monomers. DBP associates with membrane-bound C;Comment: Over 80 variants of human DBP have been identified. The three most common all
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A;Title: Complete amino acid sequence of human vitamin D-binding protein (group-specifi A;Reference number: A24066; MUID:86216223; PMID:2423133
A;Accession: A24066
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                                                                                                                                                                                                                                                                                                                                                       A;Gene: putA
C;Superfamily: proline dehydrogenase
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: putA protein
C;Species: Photobacterium leiogr
C;Date: 10-Sep-1999 #sequence_re
C;Accession: JC4661
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A; Map position: 4q12-4q13
A; Introns: 20/1; 43/2; 87/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3; 421/2; 465/3
A; Introns: 20/1; 43/2; 87/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3; 421/2; 465/3
C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: actin binding; duplication; globulin; glycoprotein; liver; plasma; polymorph
C; Keywords: actin binding; duplication; globulin; glycoprotein; liver; plasma; polymorph
F; 1-16/Domain: signal sequence #status predicted <SIG
F; 1-16/Domain: signal sequence #status predicted <SIG
F; 1-17-474/Product: vitamin D-binding protein (allele Gc1) #status
F; 17-431, E', 433-435, T', 437-474/Product: vitamin D-binding protein (allele Gc1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:U39227; NID:g1236800; PIDN:AAC43866.1; PID:g1236801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proline dehydrogenase (EC 1.5.99.8) -
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Title: Molecular basis for the three major forms of human serum vitamin D binding Reference number: A90427; MUID:79145448; PMID:218624
Reference Na90427
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154
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                                                                                    TPTELAKLVNKRSE 14
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enzyme is a multifunctional
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Pred. No. '
2; Mismatc
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Pred. No. 0.013;
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Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intrace. A;Reference number: AD3252; PMID:11756688
A;Accession: AP3445
A;Status: prelimina...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguel Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Au A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein alr0359 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec C;Accession: AF1851
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AF1851
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                                                                                                                                                                                                                                                                                                                                                                                                                        spore-cortex-lytic enzyme prepeptide precursor [imported] - Brucella melitensis (strai) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AP3445
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A;Residues: 1-248 <KUR>
A;Cross-Teferences: GB:BA000019; PIDN:BAB72317.1; PID:g17129704; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                      A;Map
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A;Residues: 1-392 <KUR>
A;Cross-references: GB:
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A;Gene: alr0359
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Matches
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                                                                          Similarity 7; Conserv
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  PTOLAKLIN 198
                                      PTELAKLVN 10
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                                                                                                                                                                                                                                 GB:AE008917; PIDN:AAL52729.1; PID:g17983559; GSPDB:GN00190
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Pred. No.
                                                                                                Score 40; DB Pred. No. 28;
                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                     intracellular pathogen Brucella melite
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lagius, S.; O'Callaghan, l
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unknown protein F22H5.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96783
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Maiti, E.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, Z.A.; Liu, Z

Kaul, S.; White, R.; Creasy, T.H.;

O.; Alonsonsons, Dewar, K

Khaykin, E.; Kim, (Maiti, R.; Marzial:

RESULT 5 A96783

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C;Accession: D88601

R;Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;seference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Note: published errata appeared in Science 283, 35, 1999; A;Note: published errata appeared in Science 283, 35, 1999; A;Note: published errata appeared in Science 283, 35, 1999; A;Note: published errata appeared in Science 283, 35, 1999; A;Note: published errata appeared in Science 283, 35, 1999; A;Note: published errata appeared in S
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A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A96783
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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A;Molecule type: DNA
A;Residues: 1-593 <STO>
                                                                                                                                                                                                                                                              R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 199

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable receptor-like protein kinase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: B84742
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A; Residues: 1-626 <STO>
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                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1124 <STO>
A;Cross-references: GB:AE002093;
                                                                                                                                                                                        A;Reference number: A84420;
A;Accession: B84742
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Gene: Y49E10.11
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Genetics
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8; Conserv
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                                        NID:g2924777; PIDN:AAC04906.1; GSPDB:GN00139
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Pred. No.
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Pred. No.
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T44732
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A;Reference number: Z22831
A;Accession: T44732
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                                                                                                                                                                                                          A;Cross-references: EMBL:X85964; NID:g757760; PIDN:CAA59946.1; PID:g757767 R;Thiele, D.; Willems, H.; Haas, M.; Krauss, H. submitted to the EMBL Data Library, October 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             片
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C;Species: Mycobacterium leprae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
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                                                                                                                 A;Cross-references: EMBL:X75356; NID:g407370; PIDN:CAA53109.1; PID:g407377 C;Superfamily: Coxiella burnetii hypothetical protein 117
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A;Experimental source: cosmid B1450
                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-117 <THI>
                                                                                                                                                                               A;Reference number: S38215
A;Accession: S38221
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A; Residues: 1-117 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                                                   Species: Coxiella burnetii
Date: 05-May-1995 #sequence_revision 01-Sep-1995
Accession: S52233; S38221
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8; Conservative
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Pred. No.
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Pred. No. 12;
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C;Species: Caenorhal C;Date: 15-Oct-1999 RESULT 10 T22716

hypothetical protein F55C5.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

#sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

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C;Accession: D98014
C;Accession: D98014
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blasze, R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; lee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; ly, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; A;Title: Genome of the Bacterium Streptococcus pne A;Reference number: A97872; MUID:21429245; PMID:11
A;Accession: D98014
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                                                                                                                                                                                                                                                                                                                 RESULT 12
D98014
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C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-699 <KUR>
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A;Residue: 1-622 <WIL>
A;Cross-references: EMBL:Z78198; PIDN:CAB01573.1; GSPDB:GN00023; CESP:F55C5.8
A;Experimental source: clone F55C5
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A;Accession: T22716
A;Status: preliminary; translated from
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A;Experimental source: strain TIGR4
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                                   A; Status: preliminary
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Molecule type: DNA
Residues: 1-701 <KUR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB Pred. No. 76; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB
Pred. No. 68;
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                                                                                   PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
76;
                                                                                                                                                                                      Blaszczak, L.; Burgett,
E.J.; Lu, J.; Matsushima
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                                                                                                     Strain R6.
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Streptococcus
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Radune, D.; Holtzapple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-Aug-2001
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                                                                                                                           R.H.;
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, McAhren,
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pneumoniae.
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A;Gene: topA
C;Superfamily: DNA topoisomerase
C;Keywords: isomerase
                   A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-1034 <KUR>
A;Residues: 1-1034 <KUR
A; Ampe, F.; Barloy-Hubler
A;Authors: Kain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
Cience 293, 668-672, 2001
A;Residues: 1-1034 <Kull
A;Residues: 1-1034 <KUR
A;Resi
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A;Residues: 1-710 <STO>
A;Cross-references: GB:AE005176; PID:g12724201; PIDN:AAK05328.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-988, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobius A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable formate dehydrogenase (EC 1.2.1.2) alpha chain FdoG [imported] - Sinorhizobium C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, Genome Res. 11, 731-753, 2001
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A; Contents: annotation
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Best Local
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;Keywords: isomerase; phosphotransferase
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7; Conserva
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Pred. No.
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Pred.
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77;
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RESULT 15
T17866
T17866
T17866
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17866
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Reference number: Z18806
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-255 <GRA>
A;Residues: 1-255 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96734.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A366L
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C;Superfamily: formate dehydrogenase
C;Keywords: oxidoreductase
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Search completed: May 21, 2004, 18:03:41 Job time: 23 secs
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699 TPEELAKEINGRA 711
                                                                                                     226 PTELKKIVGKFEE 238
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
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Match
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Gapop 10.0 , Gapext 0.5
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68
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  SwissProt_42:*
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   543
606
1210
1230
181
184
247
247
250
303
303
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 VIDB HUMAN
DPOL BR69
RVUE RALSO
TP6B PYRAE
SR68 CAESEL
TOPL LACIA
TRME MYCLE
FPRE MYCLE
FPRE MYCLE
FPRE SALTI
FALB ECOLI
FALB ECOLI
FALB SALTI
FALB SALTI
FALB SALTI
FALB ECOLI
FALB STAAM
ECRL METHO
LACR STAAM
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THIJ ECOLI
SHIT ATREN
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VILL ECOLI
SHIT ATREN
ABD4 MOUSE
ST20 CANAL
YZZ YEASTI
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  OBewb6 mycoplasma
03304 mycobacteri
08x812 e fatty oxi
p21177 e fatty oxi
p21177 e fatty oxi
0823c6 s fatty oxi
0823c6 s fatty oxi
08025 wiggleswort
099673 staphylococ
p16644 staphylococ
p16644 staphylococ
p266780 methanobact
p29570 methanobact
p29570 methanobact
p29570 methanobact
p37627 escherichia
p13208 atractaspis
p37627 escherichia
p13208 atractaspis
089016 mus musculu
092212 candida alb
p33066 saccharomyc
08ra24 thermoanaer
p12670 lycopersico
p50702 solanum com
09z7a2 chlamydia p
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008322 lactobacill
p11066 aspergillus
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Q89236 ralstonia s
Q89236 pyrobaculum
Q20822 caenorhabdi
Q9c980 lactococcus
Q8ewb6 mycoplasma
Q33064 mycoplateri
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SEQUENCE OF 17-4: MEDLINE=8621623 Schoentgen F., Moultes P.; "Complete amino (group-specific of prophys in Biophys Electric of 17-3: SEQUENCE OF 17-3: SEQUENCE OF 17-3: MEDLINE=79145448 SYMSTINE=7914549 MEDLINE=7914549 Biochemistry 18: Biochemistry 18: Biochemistry 18: BioChemistry 18: SEQUENCE OF 1-19 SEQUENCE OF 1-19 MEDLINE=88005794 Yang F., Naberham	SEQUENCE FROM N.A. SEQUENCE FROM N.A. COOKE N.E., David "Serum vitemin D-1 alpha fetoprotein J. Clin. Invest. SQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=94092730; Braun A., Kofler "Sequence and org gene."; Biochim. Biophys.	Homo sapiens (Hu Bukaryota; Metaz Mammalia; Buther NCBL TaxID=9606; [1] TaxID=9606; [1] FROM N. SEQUENCE FROM N. MEDLINE=86068030 Yang F. Brune J Yang F. Brune J "Human group-spe family.";	HUMAN 4; Q16: 71-1986 71-1986 71-1986 71-1986 71-1986 71-1986	U U U U U U U U U U U U U U U U U U U
SEQUENCE OF 17-474. MEDLINE=86216223; Pub Schoentgen F., Metz-B Jolles P.; "Complete amino acid (group-specific compo homology as in serum Biochim. Biophys. Act [5] SEQUENCE OF 17-31 AND MEDLINE=79145448; Pub Svasti J., Kurosky A. "Molecular basis for hinding protein (grou Biochemistry 18:1611- [6] USCOMMENCE OF 1-19 FROM MEDLINE=88005794; Pub Yang F., Naberhaus K.	E=86086396; N.E. David vitamin D-1 fetoprotein n. Invest. CE FROM N.A E=94092730; R. Kofler; nnce and organic and	. 0	~ F. O O O O	52.9 52.9 52.9 53.9 54.5 55.9
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olles J., n vitamin of a thre a-fetoprol (86). wwman B.H. forms of l nent).";	hird member H.; vitamin D-	Vertebrata; i; Hominidae es R.L., Nab a member of	474 AA. update) n update) (DBP) (Group-	
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PDB; 1J78; 06-FEB-02.
PDB; 1J7E; 06-FEB-02.
PDB; 1KW2; 19-JUN-02.
PDB; 1KXP; 19-JUN-02.
PDB; 1KXP; 11-FEB-03.
GlycoSuiteDB; P02774; -
SWISS-2DPAGE; P02774; -
SWISS-2DPAGE; P02774; -
Genew; HGNC:4187; GC.
MIM; 139200; -
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-i- FUNCTION: Multifunctional protein found in plasma, ascitic fluid, cerebrospinal fluid, and urine and on the surface of many cell types. In plasma, it carries the vitamin D sterols and prevents polymerization of actin by binding its monomers. DBP associates with membrane-bound immunoglobulin on the surface of b-lymphocytes and with IgG fc receptor on the membranes of T-lymphocytes.

-i- SUBCELIULAR LOCATION: Secreted.

-i- POLYMORPHISM: Over 80 variants of human DBP have been identified.

-The three most common alleles are called GC*1F, GC*1S, and GC*2.

The sequence shown is that of the GC*2 allele.

-i- SIMILARITY: Belongs to the ALB/AFP/VDB family.
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between
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Braun A., Bichlmaler R., Cleve H.;
"Molecular analysis of the gene for the human vitamin-D-binding
protein (group-specific component): allelic differences of the genetic GC types.";
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"The vitamin D-binding sequences that respond signals.";
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Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
"Characterization of mutants of the vitamin-D-binding protein/group
specific component: GC aborigine (lAl) from Australian aborigines and
South African blacks, and 2A9 from south Germany.";
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modified and this statement
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GO; GO:0005386; F:carrier activity; TAS. GO; GO:0005499; F:vitamin D binding; TAS. GO; GO:0015875; P:vitamin/cofactor transport; InterPro; IPR000264; Serum_albumin. Pfam; PF00273; transport_prot; 2. PRINTS; PR00802; SERUMALBUMIN.
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LI; K30178; CAA26938.1; -.

SL; M12654; AAA52173.1; -.

SL; S67480; AAB29423.1; JOINED.

SL; S67476; AAB29423.1; JOINED.

LL; S67478; AAB29423.1; JOINED.

SL; S67479; AAB2962.2; JOINED.

SL; S67526; AAB2962.2; ALT SEQ.

SL; S77129; AAD14250.1; ALT SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in the field and this statement is not removed. Usage by and for complete the statement is not removed.
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Polymorphism;
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                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96064739; PubMed=7592876;
Wang C.C., Yeh L.-S., Karam J.D.;
"Modular organization of T4 DNA po
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                 Wang J., Sat
Steitz T.A.;
                                MEDLINE=97358535; PubMed=9215631; Wang J., Sattar A.K., Wang C.C.,
                                                                                                    phylogenetics.";
J. Biol. Chem. 2
                                                                                                                                                                                                                   Bacteriophage RB69.
Viruses; dsDNA viruses,
T4-like viruses.
TGNI TaxID=12353;
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36, Last sequence 42, Last anno 36 (Greated)
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of T4 DNA polymerase.
a pol alpha family replication DNA polymerase
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7) (Gp43).
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InterPro; IPRO06172; DNA_pol_B.
InterPro; IPRO06134; DNA_pol_B_exo.
InterPro; IPRO06133; DNA_pol_B_exo.
Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF00136; DNA_pol_B exo; 1.
PKINTS; PR00106; DNA_pol_B
SMART; SM00486; POLBC; 1.
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PDB; 1WAL; 14-JAN-98.
PDB; 1WAL; 14-JAN-98.
PDB; 1CLQ; 28-OCT-99.
PDB; 1E1F; 29-DEC-99.
PDB; 1B8H; 05-NOV-99.
PDB; 11G9; 11-JUN-01.
PDB; 11H7; 13-JUN-01.
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2DB; 1WAH; 1
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InterPro; 1
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Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
Exonuclease; DNA-binding; 3D-structure.
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Shamoo Y., Steitz T.A.;
"Building a replisome from interacting pieces: complexed to a peptide from DNA polymerase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteriophage RB69.";
89:1087-1099(1997).
  OF COMPLEX WITH GP45
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a polymerase
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RESULT 3
RUVB RALSO
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Best Local
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                    RUVB RALSO
Q8Y236;
28-FEB-2003
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SEQUENCE
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Holliday junction DNA helicase ruvB.
RUVB OR RSC0500 OR RSC5022.
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TURN
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STRAND
                                                                                                       IF FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. RuvAB is an helicase that mediates the Holliday junction migration by localized denaturation and reanneling (By similarity).

1- SUBUNIT: Forms a complex with ruvA (By similarity).
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                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Betaproteobacteria;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum (Pseudomonas solanacearum)
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EMBL; AL646059; CAD14028.1;
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(See http://www.isb-sib.ch/announce/
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Schiex T.,
                                                                                        a collaboration
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RESULT 4
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SEQUENCE
                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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Q8ZVMO;
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Pfam; PF05491; RuvB_V; 1.
Pfam; PF05496; RuvB_V; 1.
SMART; SM00382; AAA; 1.
TIGRPAMS; TIGR0635; ruvB;
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InterPro; IPR003553; AAA_ATPase_centr.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR004605; RuvB.
InterPro; IPR008823; RuvB_C.
InterPro; IPR008824; RuvB_N.
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Complete proteome.
NP_BIND 73 80 ATP (POTENTIAL).
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STRAIN=IN2 / ATCC 51768 / DSM 7523;
STRAIN=IN2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrobaculum aerophilum.
Archaea; Crenarchaeota;
                                       HAMAP; MF_00322; -; 1.
InterPro; TPR003594; ATPbind ATPase.
InterPro; TPR003594; DNA_top6B.
InterPro; TPR005734; DNA_top6B.
Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
TIGREPAMS; TIGR01052; top6b; 1.
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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SUBUNIT: Heterotetramer of two subunits A and two subunits B
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UNCTION: Relaxes both positive and negativ
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Topoisomerase; 527 AA; 59870
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(Rel. 41, Last annotation update)
topoisomerase VI subunit B (EC 5.99.1.3) (TopoVI-B)
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39058 MW;
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DNA-binding; ATP-binding; Co
MW; 7BAADB81F8FC9D97 CRC64;
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47795DB5F7AD7DC6 CRC64;
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Q20822;
16-OCT-2001
            16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                             LACLA
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WormPep; F55C5.8; CE20875.
InterPro; IPR008941; TPR-like.
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                                                   TOP1 LACLA
Q9CG80;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                   Hypothetical protein; Signal RNA-binding.
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                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris B
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               subsequently. This ribonucleoprotein complex might interact directly with the docking protein in the ER membrane and possibly participate in the elongation arrest function (By similarity). SUBUNIT: Signal recognition particle consists of a 75 RNA molecule of 300 nucleotides and six protein subunits: SRP72, SRP68, SRP54, SRP19, SRP14 and SRP9 (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Signal-recognition-particle assembly has a crucial role in targeting secretory proteins to the rough endoplasmic reticulum membrane. SRP68 binds the 7S RNA, SRP72 binds to this complex
                                                                                                                                 499
                                                                                                                                                                                                                                                                                                                    Z78198; CAB01573.1;
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(Rel.
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                                                                 STANDARD;
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40, Last sequence update)
41, Last annotation update)
I (EC 5.99.1.2) (Omega-protein)
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nition particle 68 kDa protein (SRP68).
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Pred. No. 29;
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                                                                 PRT;
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                                                                                                                                                                                                                                        A7B8808E46169636 CRC64;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622
                                                                 710 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,
                                                                                                                                                                                  1;
                                                                                                                                                                                                            Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 527;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
 (Relaxing enzyme)
                                                                                                                                                                                                                                                                                                                                                                                    is in no
                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                              collaboration
                                                                                                                                                                                                                                                                                                                                                          ch/announce/
                                                                                                                                                                                  Gaps
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맑
                      8
                                                     Best Loc
Matches
                                                                              Query Match
                                                                                                                                                                                                                                        Pfam; PF01131; Topoisom bac; 1.
Pfam; PF0175; Toprim; 1.
Pfam; PF0136; Zf-C4 Topoisom; 3.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1Bc; 1.
SMART; SM00436; TOP1Bd; 1.
SMART; SM00493; TOPRIM; 1.
                                                                                                          ZN_FING
ZN_FING
ZN_FING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/

    -I- FUNCTION: The reaction catalyzed by topoisomerases leads to the
conversion of one topological isomer of DNA to another.
    -I- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactis ssp. lactis II1403.";
Genome Res. 11:731-753(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=IL1403;
                                                                                                                                                                                   Repeat;
                                                                                                                                                                                                              TIGRFAMs; TIGRO1051; topA_bact; 1.
PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolotin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Untwisting enzyme)
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005733;
InterPro; IPR000380;
InterPro; IPR003601;
                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE006355; AAK05328.1; PIR; F86778; F86778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weissenbach J., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006154;
                                                                                                                                                                                                somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA, followed by passage and rejoining.
SUBUNIT: Monomer (By similarity).
MISCELLANGOUS: When a topoisomerase transiently breaks a DNA
backbone bond, it simultaneously forms a protein-DNA link, in
which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
at one end of the enzyme-severed DNA strand.
SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.
518
                                                                                                                                                                                                                                                                                                                                                                                                                             P06612;
                          N
                                                                                                                                                                                   Comp
                                                     Similarity 7; Conserv
PTELGEIVNK
                         PTELAKLYNK 11
                                                                                                                                                                                               Topoisomerase; DNA-binding;
                                                                                                                      plete proteome.
595 621
635 663
670 702
321 321
                                                                                                            710 AA;
                                                                                                                                        595
635
676
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                                                      Conservative
527
                                                                                                                                                                                                                                                                                                                                                                  DNA_topI_bact.
DNA_tpisomrase.
DNAtopI_ATP_bind.
DNAtopI_DNA_bind.
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                                                                                                               80741
                                                                     57.4%;
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                                                                                                                                                                                                                                                                                                                                                       DNAtopi DNA
Toprim dom.
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                                                                                                               3
                                                      22
                                                      Score 39; DB Pred. No. 34; 2; Mismatches
                                                                                                                         C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3 (ATYPICAL).
DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorokin
                                                                                                               1268E706C38A59EB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jaillon O., Malarme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                Zinc-finger; Metal-binding;
                                                                                 1;
                                                                                 Length 710;
                                                                                                               CRC64;
                                                         Indels
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                                                         Gaps
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RESULT 7
TRMB_MYCPE
ID TRMB_M
AC Q8EWB6

TRMB_MYCPE Q8EWB6;

STANDARD;

PRT;

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FPRB
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Best Local (
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EMBL; AP004171; BAC44080.1; -.

HAWAP; MF 01057; -; 1.

InterPro; IPR004395; Cons hypoth91.

InterPro; IPR003358; Methyltransf 4; 1.

TIGRPAMS; TIGR00091; TIGR00091; 1.

TIGRPAMS; TIGR00091; TIGR00091; 1.

TYANSFERS; Methyltransferase; tRNA processing; Complete proteome.

Transferase; Methyltransferase; tRNA processing; Complete proteome.

25888 MW; FFA0D7E5F19DA310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22354719; PubMed=12466555;

Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,

Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri M.;

Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;

"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";

Nucleic Acids Res. 30:5293-5300(2002).

-I- FUNCTION: Catalyzes the formation of N(7)-methylguanine at

position 46 (m7646) in tRNA (By similarity).

-I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
homocysteine + tRNA containing N(7)-methylguanine.

-I- SIMILARITY: Belongs to the methyltransferase superfamily. TrmB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003
10-OCT-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                        MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM STRAIN=HF-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma penetrans.
Bacteria; Firmicutes;
NCBI_TaxID=28227;
MBDLINE=21128732; PubMed=11234002; Cole S.T., Eiglmeler K., Parkhill J., James K.D., Thomson N.I Cole S.T., Eiglmeler K., Parkhill J., James K.D., Harris D., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Haller R.M., Devlin K., Jagels K., Lacroix C., Maclean J., McHolroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., McHolroyd S.,
                                                                                                                                                                                                                                                                                                                     033064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methyltransferase).
                                                                                                                                                                                           Mycobacterium leprae
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                 FPRB
                                                                                                                                                                                                                                              28.FEB-2003 (Rel. 41, Created)
28.FEB-2003 (Rel. 41, Last Sequence update)
10.-CCT-2003 (Rel. 42, Last annotation update)
Probable ferredoxin/ferredoxin--NADP reductas
                                                                                                                                                                                                                                                                                                                                         FPRB
                                                                                                                                                       NCBI_TaxID=1769;
                                                                                                                          SEQUENCE
                                                                                                                                                                             Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TI-2003 (Rel. 42, Created)
TI-2003 (Rel. 42, Last sequence update)
TI-2003 (Rel. 42, Last snotation update)
(guanine-N(7)-)-methyltransferase (EC 2.
                                                                                                                                                                                                                                OR ML2134 OR MLCB57.39.
                                                                                                                                                                                                                                                                                                                                       MYCLE
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                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           PTILAKLLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                             Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                               Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                  reductase
                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1.1.33) (tRNA(m7G46)-
                                                                                                                                                                                               Actinomycetales;
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                                                                       N.R.,
       Hamlin N.,
Moule S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                    (FNR)
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RESULT 9

FADB_ECO57

ID FADB_ECO5.

'C Q84812;

28-FEB-2003 (-28-FEB-2007)

-FEB-207
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Best Local S
Matches 8
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InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR000813; 7Fe_ferredoxin.
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00037; fer4; 2.
PRINTS; PR00354; 7FE85FRDOXIN.
PRINTS; PR00356; FAD_PNR.
PRINTS; PR00368; FAD_PNR.
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DOMAIN
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: Reduced for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy L., Oliver K., Quail M.A., Rutter S., Seeger K., Simon S., S. Squares S., Stevens K., Taylor K.
                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fatty oxidation complex alpha subunit [Includes: Enoyl-CoA hydratase
(EC 4.2.1.17); Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase
(EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-
hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR OLDB OR Z5367 OR ECS4774.
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z99494; CAB16679.1; -. EMBL; AL583924; CAC31089.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: FAD; probably binds
-!- SIMILARITY: In the N-terminal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Squares S.,
Barrell B.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; T45351; T45351.
HSSP; P55907; 1XER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00198; 4FE4S_FERREI
Oxidoreductase; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ferredoxin family.
SIMILARITY: IN THE C-TERMINAL,
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8; Conserv
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PAELAKLVHAR
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115
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4FE4S FERREDOXIN; 1.
lavoprotein; NADP; FAD;
4S; Complete proteome.
83
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59712
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB Pred. No. 40; 1; Mismatches
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Simmonds M., Skelton J., Squar
K., Whitehead S., Woodward J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferredoxin +
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Enterobacteriaceae; Escherichia.

Gammaproteobacteria;

Enterobacteriales;

SEQUENCE STRAIN=01

FROM N.A 57:H7

NCBI_TaxID=83334;

MEDLINE=21074935; PubMed=11206551;

EDL933 / ATCC 700927;

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354 TEAAKLLNKQLE 365

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InterPro; IPR006108; 3HCDH C.
InterPro; IPR006108; 3HCDH N.
InterPro; IPR006176; 3HCDH C.
InterPro; IPR008927; 6DGDH C.
InterPro; IPR001753; EnCoA hydrtse.
Pfam; PF00725; 3HCDH N; 1.
Pfam; PF002737; 3HCDH N; 1.
Pfam; PF002737; 3HCDH N; 1.
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or send a
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"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).

-I- FUNCTION: FadB and fadA are the alpha and beta subunits of the multifunctional enzyme complex of the fatty acid degradation cycle (By similarity).

-I- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kirk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long. Its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001).
                                                                                                     PROSITE; PS00067; 3HCDH; 1.

PROSITE; PS00166; ENOYL COA HYDRATASE; 1.

Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase; Lyase; Isomerase; Complete proteome.

Lyase; Isomerase; Complete proteome.

SEQUENCE 729 AA; 79559 MW; C13EBBFFFA749183 CRC64;
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Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: In the N-terminal section; belongs to the hydroxyacyl-CoA dehydrogenase family. SIMILARITY: In the C-terminal section; belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydroxybutancyl-CoA.

CATALYTIC ACTIVITY: 3-cis-dodecencyl-CoA = 2-trans-dodecencyl-CoA.

PATHMAY: Fatty acid beta-oxidation cycle; third step.

SUBUNIT: Tetramer of two alpha chains and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COA + H(2)O.

CATALYTIC ACTIVITY: (S)-3-hydroxybutanoyl-CoA = (R)-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: (3S)-3-hydroxyacyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydratase/isomerase family.
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w
                                 Similarity
8; Conserv
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                                     Conservative
                                                   55.9%;
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                                     Score 38; DB
Pred. No. 52;
2; Mismatches
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52;
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                                     Indels
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Tobe T.,
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Patry oxidation complex alpha subunit [Includes: Enoyl-CoA hydr. (EC 4.2.1.7); Delta(3)-CiB-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR OLDB OR B3846.
Escherichia ~~1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Bu:
"Analysis of the Escherichia coli
from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                   Yang X.Y.H., Schulz H., Elzinga M., Yang S.Y.;
"Nucleotide sequence of the promoter and fadB gene operon and primary structure of the multifunctional oxidation protein from Becherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FADB
                                                                                                                                                                                                                                                                     CYCLE.
-i- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
                                                                                                                                                                                                                                                                                                         Biochemistry 30:6788-6795(1991).
-I- FUNCTION: FadB and fadA are the alpha and beta subunits of the multifunctional enzyme complex of the fatty acid degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary sequence of the Escherichia coli fadBA operon, encoding the fatty acid-oxidizing multienzyme complex, indicates a high degree of homology to eucaryotic enzymes."; J. Bacteriol. 172:6459-6468(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=91035260;
                This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute. There are no restrictions use, by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res.
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Nakahigashi K., Inokuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 257:771-778(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of the fadA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                      hydroxybutanoyl-CoA.

CATALYTIC ACTIVITY: 3-cis-dodecenoyl-CoA = 2-trans-dodecenoyl-CoA.

CATALYTIC ACTIVITY: 3-cis-dodecenoyl-CoA = 2-trans-dodecenoyl-CoA.

PATHWAY: Fatty acid beta-oxidation cycle; second step.

SUBUNIT: Tetramer of two alpha chains and two beta chains.

SIMILARITY: In the N-terminal section; belongs to the 3-

hydroxyacyl-CoA dehydrogenase family.

SIMILARITY: In the C-terminal section; belongs to the enoyl-CoA
                                                                                                                                                                                                                               CATALYTIC ACTIVITY:
COA + H(2)O.
                                                                                        hydratase/isomerase family.
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Escherichia.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Parkhill J., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
10-QCT-2003 (Rel. 42, Last amotation update)
Fatty oxidation complex alpha subunit [Includes: Enoyl-CoA hydratase (EC 4.2.1.17); Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR STY3577; OR T3315.
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Pfam; PF00737; 3HCDH N; 1.

Pfam; PF00378; ECH; T.

PROSITE; PS00067; 3HCDH; 1.

PROSITE; PS00166; ENOYL COA HYDRATASE;

Patty acid metabolism; Multifunctional
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InterPro; IPR006180; 3HCDH.C.
InterPro; IPR006108; 3HCDH C.
InterPro; IPR006176; 3HCDH N.
InterPro; IPR008927; 6DGDH C. like.
InterPro; IPR001753; EnCoA_hydrtse
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ECO2DBASE; G073.4; 6TH
ECO2DBASE; G073.5; 6TH
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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  SEQUENCE FROM N.A. STRAIN=TY2 / ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ceria; Gammaproteobacteria;
Salmonella.
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-> L (IN REF. 2).
-> A (IN REF. 2).
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                                                        20-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Patty oxidation complex alpha subunit [Includes: Enoyl-CoA hydratase (EC 4.2.1.17); Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR STM3983 OR STMD1.6.
Salmonella typhimurium
Bacteria
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InterPro; IPR006180; 3HCDH C.
InterPro; IPR006176; 3HCDH C.
InterPro; IPR006176; 3HCDH C.
InterPro; IPR001753; EnCoA_hydrtse.
Pfam; pP00725; 3HCDH; 2.
Pfam; pP02737; 3HCDH; 1.
Pfam; pP02737; 3HCDH; 1.
Pfam; pP00378; ECH; I.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
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-i- FUNCTION: FadB and fadA are the alpha multifunctional enzyme complex of the
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Deng W., Liou S.-I
Burland V., Kodoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by the company of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - I - CATALYTIC ACTIVITY:
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EMBL; AE016845; AA070843.1; -.
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                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY:
PATHWAY: Fatty acid
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CATALYTIC ACTIVITY: (
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8; Conserv
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R., Plunkett G. III,
Hanni V., Schwartz D.
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id beta-oxidation cycle; third step.
of two alpha chains and two beta chains (By
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[1] SEQUENCE

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InterPro; IPRO06180; 3HCDH C.
InterPro; IPRO06176; 3HCDH N.
InterPro; IPRO06176; 3HCDH N.
InterPro; IPRO01753; EnCoA_hydrtse.
InterPro; IPRO01753; EnCoA_hydrtse.
InterPro; IPRO01753; EnCOA_hydrtse.
Pfam; PF007725; 3HCDH, 2.
Pfam; PF00378; ECH; 1.
Pfam; PF00378; ECH; 1.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
FROSITE; PS00166; ENOYL COA HYDRATASE; 1.
FRATCY acid metabolism; Multifunctional en
Lyase; Isomerase; Complete proteome.
SEQUENCE 729 AA; 79594 MW; 90A6EAB578
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EMBL; AE008886; AAL22827.1;
StyGene; SG?????; fadB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LT2 / SGSC1412 / ATCC /vv/2
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
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European Bioinformatics Institute. Th
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydroxybutanoyl-COA.

CATALYTIC ACTIVITY: 3-cis-dodecenoyl-COA = 2-trans-dodecenoyl-COA.

PATHWAY: Fatty acid beta-oxidation cycle; third step.

SUBUNIT: Tetramer of two alpha chains and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: In the N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cycle (By similarity).
CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydratase/isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydroxyacyl-CoA dehydrogenase family.
SIMILARITY: In the C-terminal section; belongs to the enoyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multifunctional enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CoA + H(2)O
                                                                                                                                                                                                                                                          354
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                                                                                                                                                                                                                                                                                                                                                       8; Conserv
                                                                                                                                                                                                                                                       TEAAKLLNKQLE 365
                                                                                                                                                                                                                                                                                                       TELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                          Conservative
(Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation updat
(Rel. 42, Last annotation edat)
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SGSC1412 / ATCC 700720;
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and fadA are the alpha lenzyme complex of the
                                                                                                                                                                                                                                                                                                                                                                                  55.9%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (3S) -3-hydroxyacyl-CoA =
                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No.
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90A6EAB57871582D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  section; belongs to
on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                     DB
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme; Oxidoreductase;
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  factor)
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     (RRF)
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L outstation -
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N [1]

REQUENCE FROM N.A.

REDIINE=21311952; PubMed=11418146;

RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matbumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Kanamori M., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Sekimizu K., Yamashita A., Oshima K., Furuya K., Yoshino C., Shib

RA Kanehisa M., Yamashita A., Hayashi H., Hiramatsu K.;

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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Best Local S
Matches
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099873;
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Lactose phosphotransferase system repressor.
LACR OR SAV2196 OR SA1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD004103; RRF; 1.
TIGRPAMs; TIGR00456; frr; 1.
Protein biosynthesis; Complete
SEQUENCE 185 AA; 21650 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRR OR WIGBR3890.
Wigglesworthia glossinidia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB063522; BAC24535.1;
HAMAP; MF_00040; -; 1.
InterPro; IPR002661; RRF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=22297718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01765; RRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flies, Wigglesworthia glossinidia.";
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=158878, 158879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Genet. 32:402-407(2002).

FUNCTION: Responsible for the release of ribosomes f RNA at the termination of protein biosynthesis. May efficiency of translation by recycling ribosomes fro translation to another (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: Belongs to the RRF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
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Pred. No. 20;
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C71569E7155DECFD CRC64;
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, Hosoyama A.,
vaito C.,
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                                                                                                                                                                                                                                               Kobayashi I.,
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RESULT 15
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DT 01-AUG
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DE LACTO
OS Staphy
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RN (1)
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P16644;
                                                                                                 Oskouian B., Stewart G.C.,
"Repression and catabolite repression of the lactose operon of
Staphylococcus aureus";
J. Bacteriol. 172:3804-3812(1990).
- FUNCTION: Repressor of the lactose catabolism operon. Gald
- Phosphate is the inducer.
- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22040717; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi J. Baba T., Taman N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K., Yamamoto K., Hiramatsu K., "Genome and virulence determinants of high virulence community-"acquired MESA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620, 1280;
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DNA BIND 20
SEQUENCE 251 AA;
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InterPro; IPR009058; Wing_hlx_DNA_bnd.
Pfam; PF00455; deoR; 1.
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-I- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactose phosphotransferase system LACR OR MW2122.
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                                                                                                                                                                                                                                                                                                                                       MEDLINE=90299802; PubMed=2163387;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RN4220
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain MW2), and
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PROSITE; PS00894; HTH_DEOR_FAMILY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ancet 359:1819-1827(2002).
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   It is produced through a collaboration
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                                                                                                                                                                                                                                             EMBL; AP004829; BAB95987.1; -.
EMBL; M32103; AAA67854.1; -.
PIR; A44506, A44506.
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DNA_BIND 20
SEQUENCE 251 AA;
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SMART; SM00420; HTH DEOR; 1.
PROSITE; PS00894; HTH DEOR FAMILY; 1.
Lactose metabolism; Transcription regulation; Repressor; DNA-binding;
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Pfam; PF00455; deoR; 1.
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EIAKLVNKK 17
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Search completed: May 21, Job time : 13 secs 2004, 18:02:16

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Copyright (c) 1993 - 2004 Compugen Ltd.
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                          Qsuns2 homo sapien Qsus2 homo sapien Qsus44 bradyrhizob Qrzvt8 brachydanio Qszu6 anabaena sp Qsd9i0 vibrio vuln Q87c79 xylella fas Qrw159 bordetella Qrw152 bordetella Qrw98 bordetella Qrw98 bordetella Qrw98 bordetella gsu67440 chimpanzee Qsyfh4 brucella su Qsfr17 arabidopsis
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Q51873 photobacter
Q9uns2 homo sapien
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Primary structure of cold-adapted alkaline phosphatase from a Vibrio sp., as deduced from the nucleotide sequence.";

Biochim. Biophys. Acta 0:0-0(2001).

EMBL; AP352014; AAX94204.1; -.

R GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001952; Alk phosphtse.

Pfam; PF00245; alk phosphtse.

Pfam; PF00245; alk phosphtse; 1.

PRINTS; PR00113; ALKPHHYTASE.

R PROSITE; PR00113; ALKPHEYTASE.

PROSITE; PS00123; ALKALINE PHOSPHATASE; 1.

RR PROSITE; PS00123; ALKALINE PHOSPHATASE; 1.

SEQUENCE 521 AA; 57384 MW; 0DC4930DAD9CF192 CRC64;
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Best Local Similarity
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Vibrio sp. G15-21.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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Pred. No. 5.
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01-NOV-1996
01-JUN-2003
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
COP9 complex subunit 3 (COP9 (Constitutive PHOTOMORPHOGENIC,
ARABIDOPSIS, homolog) subunit 3) (JAB1-containing signalosome subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin J.W., Yu K.Y., Chen H.Y., Weng S.F.;
"Regulatory region with putA gene of proline dehydrogenase that links to the lum and the lux operons in Photobacterium leiognathi.";
Biochem. Biophys. Res. Commun. 219:868-875(1996).
EMBL; U39227; AAC43866.1; -
                                                                                                          MEDLINE-99206679; PubMed=10191102; Potocki L., Chen K.-S., Lupski J.R.; "Subunit 3 of the COP9 signal transduction complex plants to humans and maps within the smith-magenis region in 17p11.2."; Genomics 57:180-182(1999).
                                                                                                                                                                                                                     COPS3 OR SGN3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                   Genomics [2]
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Vibrionaceae; Photobacterium.
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MEDLINE=98194867; PubMed=9535219; Seeger M., Kraft R., Ferrell K., Schade R., Gordon C., Naumann M.,
                                                                            SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                       Strausberg R.;
Submitted (JAN-2001)
                                                                                                                                                                              TISSUE=Brain;
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                                 SEQUENCE OF 21-423 FROM N.A.
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Pred. No.
                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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, Dubiel W.;
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PASEB J. 12:469-478 (1998).

EMBL; APO98109; AAD41247.1; -.

EMBL; BC001991; AAH01891.1; -.

EMBL; APO31647; AAC14197.1; -.

Genew; HGNC:2239; COPS3.

GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0009416; P:response to light; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007165; P:TAS.
GO; GO:000717; PCI.
                       Q7ZVT8;
Q7ZVTB;
01-JUN-2003
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Similar to C
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Q89E44;
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SEQUENCE
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MEDLING=22484998; PubMed=12597275;
MEDLING=22484998; PubMed=12597275;
MEDLING=22484998; PubMed=12597275;
Mancho T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP005961; BAC52508.1; -. GO; GC:0006118; P:electron transport; InterPro; IPR001128; Cytochrome_P450. Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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STRAIN=USDA 110;
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COPP constitutive photomorphogenic homolog
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VV12621.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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EMBL; BC045415; AAH45415.1; -.
InterPro; IPR000717; PCI:
InterPro; IPR008941; TPR-1ike.
Pfam; PP01399; PCI; 1.
SMART; SM00088; PINT; 1.
SMART; SM00088; PINT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical ALR0359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9nza8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF1851; AF1851.
                                                                                                                                                                                                                                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP003582; BAB72317.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
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9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAELRALVNKHSE 284
                                                                                                                                                                                                                                                                                                                                                                                                         PTEIEKLVQKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTELAKLVNKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l protein;
248 AA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TIRMBLrel. 20, Created)
(TIRMBLrel. 20, Last sequence update)
(TIRMBLrel. 24, Last annotation update)
L protein Alr0359.
                                     (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation updat)
(Ized conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                           PRELIMINARY;
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27298 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 39;
); Mismatches
                                                                                                                                                                                                                           PRT;
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OAE81453DD0E9991
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                                                                           update)
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hima K., Kimura T.,
A., Muraki A.,
a M., Yamada M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  RX MEDLINE=22421331; PubMed=12533478;
RX WEDLINE=22421331; PubMed=12533478;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA Taktta M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA Coutinho L.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighteri E.F., Kishi L.T.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighteri E.F., Kishi L.T.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RA Kitajima J.P.;
                                                                                                    Query Match
Best Local S
Matches 8
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Best Local
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01-JUN-2003 (TrEMBLrel. 24, Lasi
01-JUN-2003 (TrEMBLrel. 24, Lasi
Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016805; AA010970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=672;
                                                                                                                                                                                                              Hypothetical protein; Complete SEQUENCE 135 AA; 15769 MW;
                                                                                                                                                                                                                                                                 J. Bacteriol. 185:1018-1026(2003).
EMBL; AE012557; AA029065.1; -.
                                                                                                                                                                                                                                                                                                                                                       disease and citrus variegated
                                                                                                                                                                                                                                                                                                                                                          "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                             fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=183190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylella fastidiosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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28
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                                                                                                       Similarity
8; Conserv
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                               TELAKLVNKRSE 14
TDVAKLVNVKNE 39
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                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43925 MW;
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                                                                                                                                58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n Temeculal / ATCC 700964).
Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
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••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E2F5F951FA95E132 CRC64;
                                                                                                                                                                                                                proteome.
7C540986E7B99455 CRC64;
                                                                                                            Mismatches
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                                                                                                                                      DB 27;
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                                                                                                                                                             16;
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                                                                                                                                                          Length 135;
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RESULT 9
Q7WL59
ID Q7WL59

PRELIMINARY;

PRT;

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8

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RESULT 10
Q7W7S2
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                                                                                         RP SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

KC STRAIN=12822 / ATCC BAA-587;

KMEDLINE=22827954; PubMed=12910271;

KMEDLINE=22827954; PubMed=128271;

KMEDLINE=22827954; PubMed=128271;

KMEDLINE=22827954; PubMed=128271;

KMEDLINE=22827954; PubMed=128271;

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KMEDLINE=
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Best Local S
Matches 7
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A Parkhill J., Sebalhia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E.; Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

A Kabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

A Rabbinowitsch E., Rutter S., Saunders D., Seeger K.,

A Mabinowitsch E., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parrapertussis and Bordetella bronchiseptica.";

Bordetella parapertussis and Bordetella bronchiseptica.";

Bell; Excholer CAB32387.1;

Complexe Porter Came
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01-OCT-2003
01-OCT-2003
01-OCT-2003
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SEQUENCE
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
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Bacteria, Proteobacteria,
Alcaligenaceae, Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Alcaligenaceae; Bordetelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7W7S2;
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                                                                   BX640430; CAE37737.1; -.
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7; Conserv
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162 AA;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
anscriptional regulator (MarR family).
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   18047 MW;
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Betaproteobacteria; Burkholderiales;
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Last annotation update)
gulator (MarR family).
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Pred. No.
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   96814512C9198346 CRC64;
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Quail M.A.,
                                                                                                                                                                                                                                                  Stevens K.,
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K STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

K MEDLINE-22827954; PubMed-12910271;

K MEDLINE-22827954; PubMed-12910271;

K MEDLINE-22827954; PubMed-12910271;

K Parkhill J., Sebahha M., Preston A., Murphy L.D., Thomson N.,

K Parkhill J., Sebahha M., Preston A., Murphy L.D., Thomson N.,

K A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

K Cerdeno-Tarraga A.M., Temple L., James K., Hason N., Cherevach I.,

K A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

K A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

K A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

K A Chillingworth T., Collins M., Hamalin N., Hauser H., Holroyd S., Jagels K.,

K A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

K A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

K A Feltwell T., Goble A., Hamlin N., Sunders M., Saunders D., Seeger K.,

K A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

K R Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

K R Rabbinowitsch E., Stelton J., Squares R., Squares S., Stevens K.,

K R Rabbinowitsch E., Barrell B.G., Maskell D.J.;

Moria L., Whitehead S., Barrell B.G., Maskell D.J.;

Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).
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Best Local S
Matches
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Best Local S
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Q7VWG8;
01-OCT-2003
                                                                                                                                                                                                                                      Q87440;
Q87440;
01-NOV-1996
                                                                                                                                                                          ENV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
SEQUENCE
                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; B
Alcaligenaceae; Bordetella.
             SEQUENCE FROM N.A.

MEDLINE=95193252; PubMed=7886956;

Rudensey L.M., Kimata J.T., Benveniste R.E., Overbaugh J.;

Rudensey L.M., Kimata J.T., Benveniste R.E., Overbaugh J.;

"Progression to AIDS in macaques is associated with changes in

replication, tropism, and cytopathic properties of the simian

immunodeficiency virus variant population.";
                                                                                                                                            Chimpanzee
Viruses; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella
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 Virology
                                                                                                                         NCBI_TaxID=11723;
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                                                                                                                                           ee immunodeficiency
Retroid viruses; Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 AA; 18047 MW;
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70.0%;
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25, Last annotation update)
regulator (MarR family).
                                                                                                                                            cy virus (SIV(cpz)) (CIV)
Retroviridae; Lentivirus
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Pred. No.
                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT 13
Q8YFH4
ID Q8YFH
AC Q8YFH
DT 01-MA
DT 01-JU
DE Spore
GN EMEII
OS Bruce
OC Bruce
OC Bruce
OC Bruce
OX NCBI_
RP SEQUI
RC STRAJ
AX MEDLI
RA JABIA
RA J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N [1]

RDGUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAIN-16M / ATCC 23456 / Blotype 1;

RX MEDLINE-20020109; PubMed=11756688;

RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

RA Jablonski L., Larseen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Haselkorn R., Kyrpides N., Overbeek R.;

RT "The genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

Brucella melitensis.";

Brucella melitensis.";
RESULT 14
QBG2ES
ID QBG2E
AC QBG2E
AC QBG2E
DT 01-WS
DT 01-WS
DT 01-WS
DT 01-WS
DT 01-WS
CONSEG
GN BROSS
OS Bruce
OC Barte
OC Bruce
OC Bruce
OC NCEN
RN [1]
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Best Local S
Matches 8
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Best Local
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Q8YFH4;
01-MAR-2002
01-MAR-2002
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NON TER
SEQUENCE
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella. NCBI_TaxID=29461;
                                                                                                                                                                     QBGZE5 PRELIMINARY; PRT; 429 AA.
QBGZE5;
Q1-MAR-2003 (TEMBLrel. 23, Created)
O1-MAR-2003 (TEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
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                                                                                                                        Conserved hypothetical BR0378.
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Brucellaceae; Brucella.
                                                                                                   Brucella suis.
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(TrEMBLrel. 24, Last annotation update)
-- oric enzyme PREPEPTIDE precursor.
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Pred. No. 82;
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barristead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC025814; AAG12682.1; -.

EMBL; AC025814; AAG12682.1; -.

EMBL; AC025814; F:catalytic activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

Ffam; PP02716; Isoflavone_redu; 1.
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01-MAR-2001
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       animal and plant pathogens and symbionts."; Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
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Paulsen I.T., Seshadri R., Nelson K.E.,
                                                                                                                                                                                                                          SEQUENCE
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see 8; Conserv
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Pred. No. 1.3e+02;
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Search completed: May 21, 2004, 18:03:09 Job time: 42 secs